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RAW SEQUENCE LISTING DATE: 08/19/2004
 PATENT APPLICATION: US/10/656,725 TIME: 17:05:21

Input Set : N:\AMC\US10656725.raw
 Output Set: N:\CRF4\08192004\J656725.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:
 2 (i) APPLICANT: Goli, Surya K.
 3 Hillman, Jennifer L.
 4 Murry, Lynn E.
 5 (ii) TITLE OF INVENTION: NOVEL HUMAN CYTOKINE/STEROID
 6 RECEPTOR PROTEIN
 7 (iii) NUMBER OF SEQUENCES: 4
 8 (iv) CORRESPONDENCE ADDRESS:
 9 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 10 (B) STREET: 3174 Porter Drive
 11 (C) CITY: Palo Alto
 12 (D) STATE: CA
 13 (E) COUNTRY: US
 14 (F) ZIP: 94304
 15 (v) COMPUTER READABLE FORM:
 16 (A) MEDIUM TYPE: Diskette
 17 (B) COMPUTER: IBM Compatible
 18 (C) OPERATING SYSTEM: DOS
 19 (D) SOFTWARE: FastSEQ Version 2.0
 20 (vi) CURRENT APPLICATION DATA:
 C--> 21 (A) APPLICATION NUMBER: US/10/656,725
 C--> 22 (B) FILING DATE: 04-Sep-2003
 23 (C) CLASSIFICATION: 530
 24 (vii) PRIOR APPLICATION DATA:
 25 (A) APPLICATION NUMBER: US/08/822,264
 26 (B) FILING DATE: 20-MAR-1997
 27 (viii) ATTORNEY/AGENT INFORMATION:
 28 (A) NAME: Billings, Lucy J
 29 (B) REGISTRATION NUMBER: 36,749
 30 (C) REFERENCE/DOCKET NUMBER: PF-0233 US
 31 (ix) TELECOMMUNICATION INFORMATION:
 32 (A) TELEPHONE: 415-855-0555
 33 (B) TELEFAX: 415-845-4166
 34 (C) TELEX:
 35 (2) INFORMATION FOR SEQ ID NO: 1:
 36 (i) SEQUENCE CHARACTERISTICS:
 37 (A) LENGTH: 220 amino acids
 38 (B) TYPE: amino acid
 39 (C) STRANDEDNESS: single
 40 (D) TOPOLOGY: linear
 41 (vii) IMMEDIATE SOURCE:
 42 (A) LIBRARY: CONUTUT101



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(B) CLONE: 2504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

43 Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
44 1 5 10 15
45 Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
46 20 25 30
47 Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
48 35 40 45
49 Asp Gln Pro Ala Ala Ser Gly Asp Arg Thr Thr Thr Xaa Pro Pro Pro
50 50 55 60
51 Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
52 65 70 75 80
53 Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
54 85 90 95
55 Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
56 100 105 110
57 Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
58 115 120 125
59 Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
60 130 135 140
61 Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp Trp Glu Ser Gln Phe
62 145 150 155 160
63 Thr Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu
64 165 170 175
65 Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ser Arg
66 180 185 190
67 Lys Asn Val Lys Ala Phe Ser Gly Ser Ile Ser Xaa Xaa Tyr Phe Ala
68 195 200 205
69 Lys Ser Phe Val Thr Val His Xaa Val Phe Lys Thr
70 210 215 220

```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 788 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: CONUTUT101

(B) CLONE: 2504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

84 GCCGCCGAAC CCCGCGCGCC ACTCGCTCGC TCAGAGGGAG GAGAAAGTGG CGAGTTCCGG 60
85 ATCCCTGCCT AGCGCGGCCC AACCTTTACT CCAGAGATCA TGGCTGCCGA GGATGTGGTG 120
86 GCGACTGGCG CCGACCCAAG CGATCTGGAG AGCGGCGGGC TGCTGCATGA GATTTTCACG 180
87 TCGCCGCTCA ACCTGCTGCT GCTTGGCCTC TGCATCTTCC TGCTCTACAA GATCGTGCGC 240
88 GGGGACCAGC CGGCGGCCAG CGGCGACAGG ACGACGACGA NGCCGCCCCC TCTGCCCCGC 300
89 CTCAAGCGGC GCGACTTCAC CCCC GCCGAG CTGCGGCGCT TCGACGGCGT CCAGGACCCG 360
90 CGCATACTCA TGGCCATCAA CGGCAAGGTG TTCGATGTGA CCAAAGGCCG CAAATTCTAC 420
91 GGGCCCGAGG GGCCGTATGG GGTCTTTGCT GGAAGAGATG CATCCAGGGG CCTTGCCACA 480
92 TTTTGCCTGG ATAAGGAAGC ACTGAAGGAT GAGTACGATG ACCTTTCTGA CCTCACTGCT 540

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```

93  GCCCAGCAGG AGACTCTGAG TGAAGGAGGG TCTCAGTTCA CTTTCAAGTA TCATCACGTG      600
94  GGCAAAGTGC TGAAGGAGGG GGAGGAGCCC ACTGTGTACT CAGATGAGGA AGAACCAAAA      660
95  GATGAGAGTT CCCGGAAAAA TGTTAAAGCA TTCAGTGGAA GTATATCTAT NNTGTATTTT      720
96  GCAAAATCAT TTGTAACAGT CCACTNTGTC TTAAAACAT AGTGTTACAA TATTTAGAAA      780
97  GTTTGAGC                                     788

```

99 (2) INFORMATION FOR SEQ ID NO: 3:

100 (i) SEQUENCE CHARACTERISTICS:

101 (A) LENGTH: 223 amino acids

102 (B) TYPE: amino acid

103 (C) STRANDEDNESS: single

104 (D) TOPOLOGY: linear

105 (vii) IMMEDIATE SOURCE:

106 (A) LIBRARY: GenBank

107 (B) CLONE: 158818

108 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

109 Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Glu Leu
110 1          5          10          15
111 Glu Gly Gly Gly Leu Leu Gln Glu Ile Phe Thr Ser Pro Leu Asn Leu
112          20          25          30
113 Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
114          35          40          45
115 Asp Gln Pro Gly Ala Ser Gly Asp Asn Asp Asp Asp Glu Pro Pro Pro
116          50          55          60
117 Leu Pro Arg Leu Lys Pro Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg
118 65          70          75          80
119 Tyr Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
120          85          90          95
121 Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
122          100          105          110
123 Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
124          115          120          125
125 Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
126          130          135          140
127 Leu Thr Pro Ala Gln Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe
128 145          150          155          160
129 Ser Ser Pro Ser Ser Thr Ile Thr Trp Gly Lys Leu Leu Glu Gly Ala
130          165          170          175
131 Glu Glu Pro Ile Val Tyr Ser Asp Asp Glu Glu Gln Lys Met Arg Leu
132          180          185          190
133 Leu Gly Arg Val Thr Glu Ala Val Ser Gly Ala Tyr Leu Phe Leu Tyr
134          195          200          205
135 Phe Ala Lys Ser Phe Val Thr Phe Gln Ser Val Phe Thr Thr Trp
136          210          215          220

```

138 (2) INFORMATION FOR SEQ ID NO: 4:

139 (i) SEQUENCE CHARACTERISTICS:

140 (A) LENGTH: 194 amino acids

141 (B) TYPE: amino acid

142 (C) STRANDEDNESS: single

143 (D) TOPOLOGY: linear

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144 (vii) IMMEDIATE SOURCE:

145 (A) LIBRARY: GenBank

146 (B) CLONE: 1657409

147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

148 Met Ala Ala Glu Asp Val Ala Ala Thr Gly Ala Asp Pro Ser Glu Leu
149   1           5           10           15
150 Glu Gly Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
151           20           25           30
152 Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
153           35           40           45
154 Asp Gln Pro Ala Ala Ser Asp Ser Asp Asp Asp Glu Pro Pro Pro Leu
155           50           55           60
156 Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg Phe
157           65           70           75           80
158 Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys Val
159           85           90           95
160 Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro Tyr
161           100          105          110
162 Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys
163           115          120          125
164 Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp Leu
165           130          135          140
166 Thr Pro Ala Gln Gln Glu Thr Leu Asn Asp Trp Asp Ser Gln Phe Thr
167           145          150          155          160
168 Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu Pro
169           165          170          175
170 Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ala Arg Lys
171           180          185          190
172 Asn Asp

```